GGGGCCACGG GGGGTGCGCC GGCGCGCGGT AGCGCGGCC CCTCAGTGCA CAATGGCCAG 60
AGCAGGCGGC GGAGCCCCAG CCCCACCCAG TGCGGAGCGC GCCGCGAGCC CCGCCGCAAG 120
CTGAGCGCCT CCGCCCGCCA GGCGCGCCGG CGCCGGGCCA TGTACTCGGG GAACCGCAGC 180
GGCGGCCACG GCTACTGGGA CGGCGGCGGG GCCGCGGGCG CTGAGGGGCC GGCGCCGGCG 240
GGGACACTGA GCCCCGCGCC CCTCTTCAGC CCCGGCACCT ACGAGCGCCT GGCGCTGCTG 300
CTGGGCTCCA TTGGGCTGCT GGGCGTCGGC AACAACCTGC TGGTGCTCGT CCTCTACTAC 360
AAGTTCCAGC GGCTCCGCAC TCCCACTCAC CTCCTCCTGG TCAACATCAG CCTCAGCGAC 420
CTGCTGGTGT CCCTCTTCGG GGTCACCTTT ACCTTCGTGT CCTGCCTGAG GAACGGCTGG 480
GTGTGGGACA CCGTGGGCTG CGTGTGGGAC GGGTTTAGCG GCAGCCTCTT CGGGATTGTT 540
TCCATTGCCA CCCTAACCGT GCTGGCCTAT GAACGTTACA TTCGCGTGGT CCATGCCAGA 600
GTGATCAATT TTTCCTGGGC CTGGAGGGCC ATTACCTACA TCTGGCTCTA CTCACTGGCG 660
TGGGCAGGAG CACCTCTCCT GGGATGGAAC AGGTACATCC TGGACGTACA CGGACTAGGC 720
TGCACTGTGG ACTGGAAATC CAAGGATGCC AACGATTCCT CCTTTGTGCT TTTCTTATTT 780
CTTGGCTGCC TGGTGGTGCC CCTGGGTGTC ATAGCCCATT GCTATGGCCA TATTCTATAT 840
TCCATTCGAA TGCTTCGTTG TGTGGAAGAT CTTCAGACAA TTCAAGTGAT CAAGATTTTA 900
AAATATGAAA AGAAACTGGC CAAAATGTGC TTTTTAATGA TATTCACCTT CCTGGTCTGT 960
TGGATGCCTT ATATCGTGAT CTGCTTCTTG GTGGTTAATG GTCATGGTCA CCTGGTCACT 1020
CCAACAATAT CTATTGTTTC GTACCTCTTT GCTAAATCGA ACACTGTATA CAATCCAGTG 1080
ATTTATGTCT TCATGATCAG AAAGTTTCGA AGATCCCTTT TGCAGCTTCT GTGCCTCCGA 1140
CTGCTGAGGT GCCAGAGGCC TGCTAAAGAC CTACCAGCAG CTGGAAGTGA AATGCAGATC 1200
AGACCCATTG TGATGTCACA GAAAGATGGG GACAGGCCAA AGAAAAAAGT GACTTTCAAC 1260
TCTTCTTCCA TCATTTTTAT CATCACCAGT GATGAATCAC TGTCAGTTGA CGACAGCGAC 1320
AAAACCAATG GGTCCAAAGT TGATGTAATC CAAGTTCGTC CTTTGTAGGA ATGAAGAATG 1380
GCAACGAAAG ATGGGGCCTT AAATTGGATG CCACTTTTGG ACTTTCATCA TAAGAAGTGT 1440
CTGGAATACC CGTTCTATGT AATATCAACA GAACCTTGTG GTCCAGCAGG AAATCCGAAT 1500
TGCCCATATG CTCTTGGGCC TCAGGAAGAG GTTGAAC (SEQ ID NO:1) 1537

FIG.1

```
  1 MYSGNRSGGH GYWDGGGAAG AEGPAPAGTL SPAPLFSPGT YERLALLLGS
 51 IGLLGVGNNL LVLVLYYKFQ RLRTPTHLLL VNISLSDLLV SLFGVTFTFV
101 SCLRNGWVWD TVGCVWDGFS GSLFGIVSIA TLTVLAYERY IRVVHARVIN
151 FSWAWRAITY IWLYSLAWAG APLLGWNRYI LDVHGLGCTV DWKSKDANDS
201 SFVLFLFLGC LVVPLGVIAH CYGHILYSIR MLRCVEDLQT IQVIKILKYE
251 KKLAKMCFLM IFTFLVCWMP YIVICFLVVN GHGHLVTPTI SIVSYLFAKS
301 NTVYNPVIYV FMIRKFRRSL LQLLCLRLLR CQRPAKDLPA AGSEMQIRPI
351 VMSQKDGDRP KKKVTFNSSS IIFIITSDES LSVDDSDKTN GSKVDVIQVR
401 PL (SEQ ID NO:2)
```

FIG.2

```
GGGGCCACGG GGGGTGCGCC GGCGCGCGGT AGCGCGGGCC CCTCAGTGCA CAATGGCCAG   60
AGCAGGCGGC GGAGCCCCAG CCCCACCCAG TGCGGAGCGC GCCGCGAGCC CCGCCGCAAG  120
CTGAGCGCCT CCGCCCGCCA GGCGCGCCGG CGCCGGGCCC ATG TAC TCG GGG AAC    174
                                           MET TYR SER GLY ASN
                                            1               5

CGC AGC GGC GGC CAC GGC TAC TGG GAC GGC GGC GGG GCC GCG GGC GCT    222
ARG SER GLY GLY HIS GLY TYR TRP ASP GLY GLY GLY ALA ALA GLY ALA
                10                  15                  20

GAG GGG CCG GCG CCG GCG GGG ACA CTG AGC CCC GCG CCC CTC TTC AGC    270
GLU GLY PRO ALA PRO ALA GLY THR LEU SER PRO ALA PRO LEU PHE SER
            25                  30                  35

CCC GGC ACC TAC GAG CGC CTG GCG CTG CTG CTG GGC TCC ATT GGG CTG    318
PRO GLY THR TYR GLU ARG LEU ALA LEU LEU LEU GLY SER ILE GLY LEU
        40                  45                  50

CTG GGC GTC GGC AAC AAC CTG CTG GTG CTC GTC CTC TAC TAC AAG TTC    366
LEU GLY VAL GLY ASN ASN LEU LEU VAL LEU VAL LEU TYR TYR LYS PHE
    55                  60                  65

CAG CGG CTC CGC ACT CCC ACT CAC CTC CTC CTG GTC AAC ATC AGC CTC    414
GLN ARG LEU ARG THR PRO THR HIS LEU LEU LEU VAL ASN ILE SER LEU
70                  75                  80                  85

AGC GAC CTG CTG GTG TCC CTC TTC GGG GTC ACC TTT ACC TTC GTG TCC    462
SER ASP LEU LEU VAL SER LEU PHE GLY VAL THR PHE THR PHE VAL SER
                90                  95                  100

TGC CTG AGG AAC GGC TGG GTG TGG GAC ACC GTG GGC TGC GTG TGG GAC    510
CYS LEU ARG ASN GLY TRP VAL TRP ASP THR VAL GLY CYS VAL TRP ASP
            105                 110                 115

GGG TTT AGC GGC AGC CTC TTC GGG ATT GTT TCC ATT GCC ACC CTA ACC    558
GLY PHE SER GLY SER LEU PHE GLY ILE VAL SER ILE ALA THR LEU THR
        120                 125                 130

GTG CTG GCC TAT GAA CGT TAC ATT CGC GTG GTC CAT GCC AGA GTG ATC    606
VAL LEU ALA TYR GLU ARG TYR ILE ARG VAL VAL HIS ALA ARG VAL ILE
    135                 140                 145
```

FIG. 3A

AAT TTT TCC TGG GCC TGG AGG GCC ATT ACC TAC ATC TGG CTC TAC TCA 654
ASN PHE SER TRP ALA TRP ARG ALA ILE THR TYR ILE TRP LEU TYR SER
150 155 160 165

CTG GCG TGG GCA GGA GCA CCT CTC CTG GGA TGG AAC AGG TAC ATC CTG 702
LEU ALA TRP ALA GLY ALA PRO LEU LEU GLY TRP ASN ARG TYR ILE LEU
170 175 180

GAC GTA CAC GGA CTA GGC TGC ACT GTG GAC TGG AAA TCC AAG GAT GCC 750
ASP VAL HIS GLY LEU GLY CYS THR VAL ASP TRP LYS SER LYS ASP ALA
185 190 195

AAC GAT TCC TCC TTT GTG CTT TTC TTA TTT CTT GGC TGC CTG GTG GTG 798
ASN ASP SER SER PHE VAL LEU PHE LEU PHE LEU GLY CYS LEU VAL VAL
200 205 210

CCC CTG GGT GTC ATA GCC CAT TGC TAT GGC CAT ATT CTA TAT TCC ATT 846
PRO LEU GLY VAL ILE ALA HIS CYS TYR GLY HIS ILE LEU TYR SER ILE
215 220 225

CGA ATG CTT CGT TGT GTG GAA GAT CTT CAG ACA ATT CAA GTG ATC AAG 894
ARG MET LEU ARG CYS VAL GLU ASP LEU GLN THR ILE GLN VAL ILE LYS
230 235 240 245

ATT TTA AAA TAT GAA AAG AAA CTG GCC AAA ATG TGC TTT TTA ATG ATA 942
ILE LEU LYS TYR GLU LYS LYS LEU ALA LYS MET CYS PHE LEU MET ILE
250 255 260

TTC ACC TTC CTG GTC TGT TGG ATG CCT TAT ATC GTG ATC TGC TTC TTG 990
PHE THR PHE LEU VAL CYS TRP MET PRO TYR ILE VAL ILE CYS PHE LEU
265 270 275

GTG GTT AAT GGT CAT GGT CAC CTG GTC ACT CCA ACA ATA TCT ATT GTT 1038
VAL VAL ASN GLY HIS GLY HIS LEU VAL THR PRO THR ILE SER ILE VAL
280 285 290

TCG TAC CTC TTT GCT AAA TCG AAC ACT GTA TAC AAT CCA GTG ATT TAT 1086
SER TYR LEU PHE ALA LYS SER ASN THR VAL TYR ASN PRO VAL ILE TYR
295 300 305

GTC TTC ATG ATC AGA AAG TTT CGA AGA TCC CTT TTG CAG CTT CTG TGC 1134
VAL PHE MET ILE ARG LYS PHE ARG ARG SER LEU LEU GLN LEU LEU CYS
310 315 320 325

FIG. 3B

```
CTC CGA CTG CTG AGG TGC CAG AGG CCT GCT AAA GAC CTA CCA GCA GCT   1182
LEU ARG LEU LEU ARG CYS GLN ARG PRO ALA LYS ASP LEU PRO ALA ALA
                330                 335                 340

GGA AGT GAA ATG CAG ATC AGA CCC ATT GTG ATG TCA CAG AAA GAT GGG   1230
GLY SER GLU MET GLN ILE ARG PRO ILE VAL MET SER GLN LYS ASP GLY
            345                 350                 355

GAC AGG CCA AAG AAA AAA GTG ACT TTC AAC TCT TCT TCC ATC ATT TTT   1278
ASP ARG PRO LYS LYS LYS VAL THR PHE ASN SER SER SER ILE ILE PHE
        360                 365                 370

ATC ATC ACC AGT GAT GAA TCA CTG TCA GTT GAC GAC AGC GAC AAA ACC   1326
ILE ILE THR SER ASP GLU SER LEU SER VAL ASP ASP SER ASP LYS THR
    375                 380                 385

AAT GGG TCC AAA GTT GAT GTA ATC CAA GTT CGT CCT TTG TAGGAATGAA    1375
ASN GLY SER LYS VAL ASP VAL ILE GLN VAL ARG PRO LEU (SEQ ID NO:2)
 390                 395                 400

GAATGGCAAC GAAAGATGGG GCCTTAAATT GGATGCCACT TTTGGACTTT CATCATAAGA  1435
AGTGTCTGGA ATACCCGTTC TATGTAATAT CAACAGAACC TTGTGGTCCA GCAGGAAATC  1495
CGAATTGCCC ATATGCTCTT GGGCCTCAGG AAGAGGTTGA AC (SEQ ID NO:2)       1537
```

FIG. 3C

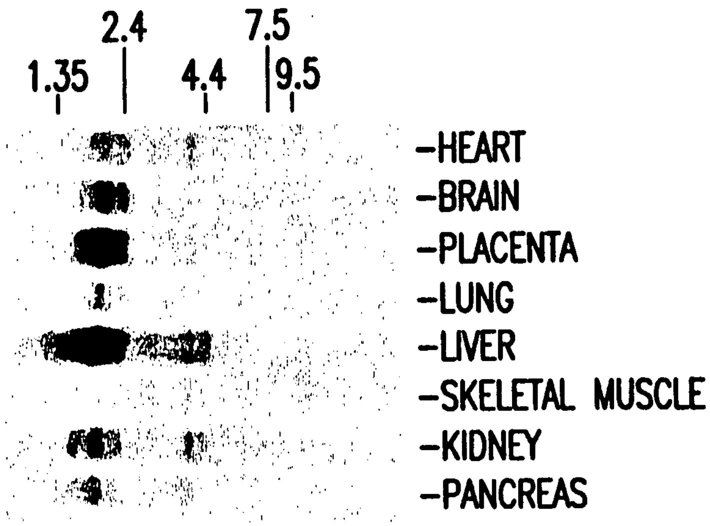

FIG.4A

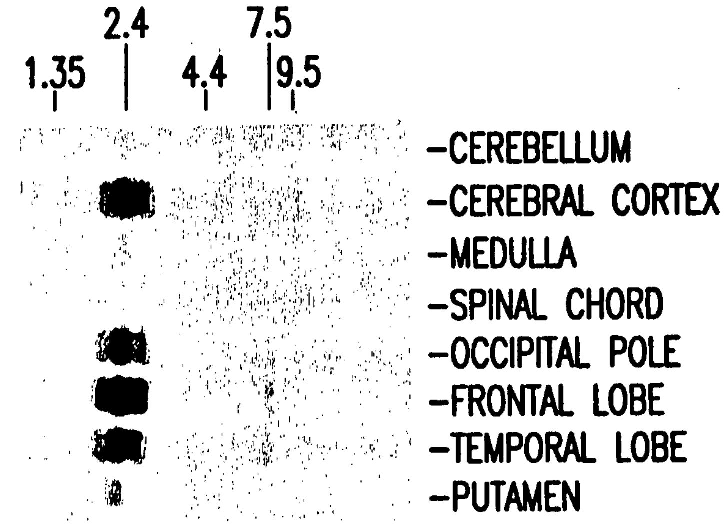

FIG.4B

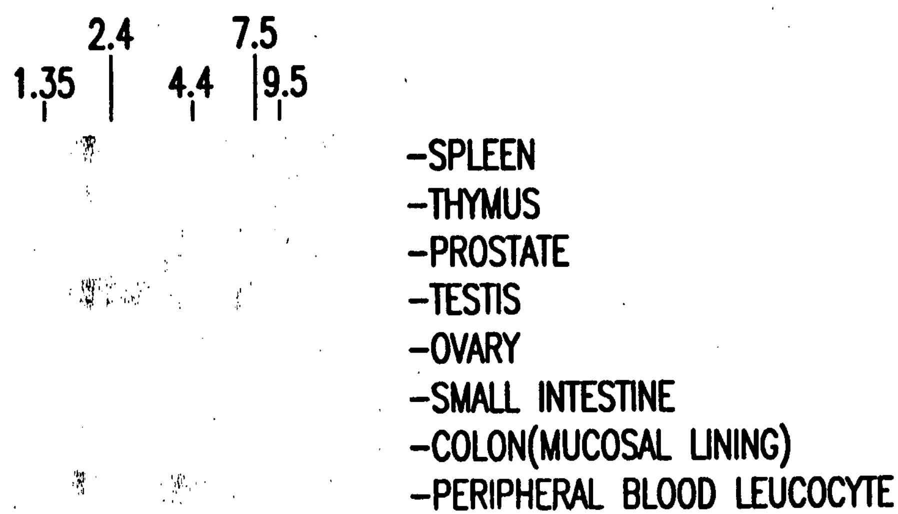

FIG.4C

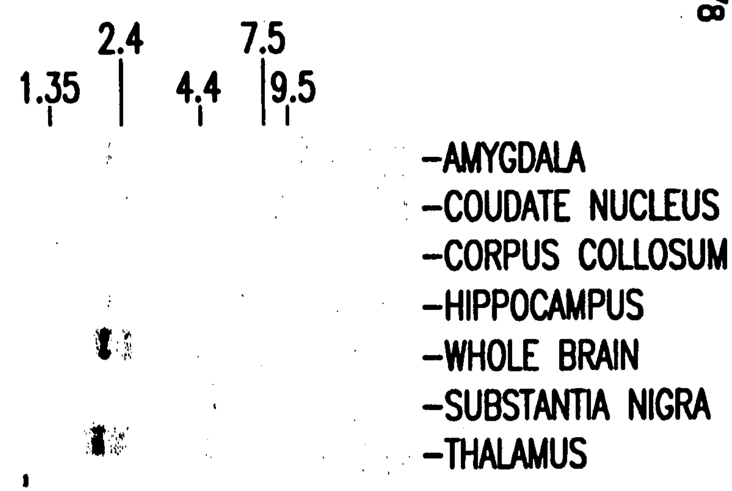

FIG.4D

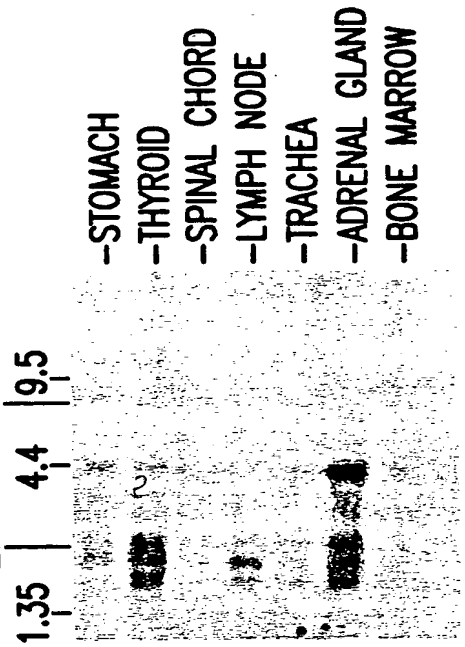

FIG.4E

```
                     10        20        30        40        50        60
RHODOPSIN  MNGTEGPNFYVPFSNATGVVRSPFEYPQYYLAEPWQFSMLAAYMFLLIVLGFPINFLTLY
                                       |  |  :  ||  :  : :||   |:|:|
HG51       NRSGGHGYWDGGGAAGAEGPAPAGTLSPAPLFSPGTYERLALLLGSIGLLGVGNNLLVLV
               10        20        30        40        50        60

                     70        80        90       100       110       120
RHODOPSIN  VTVQHKKLRTPLNYILLNLAVADLFMVLGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLG
           :  : ::|||| : :|:|:::::||:: | | | |: : |:: :|:  :||  :|| ::|
HG51       LYYKFQRLRTPTHLLLVNISLSDLLVSLFGVTFTFVSCLRNGWVWDTVGCVWDGFSGSLF
               70        80        90       100       110       120

                    130       140        150       160       170      179
RHODOPSIN  GEIALWSLVVLAIERYV-VVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLAGWSRYI
           | ::: :|:||| |||: ||    : || :     |  :::: |:::|| |: || ||:|||
HG51       GIVSIATLTVLAYERYIRVVHARVINFSW----AWRAITYIWLYSLAWAGAPLLGWNRYI
               130       140       150          160       170       180

           180       190       200       210       220       230
RHODOPSIN  PEGLQCSCGIDYYTLKPEVNNESFVIYMFVVHFTIPMIIIFFCYGQLVFTVKEAAA----
            :     :| :|: :    ::|: |||:::|:  :::|: :|   |||:::::::
HG51       LDVHGLGCTVDWKS--KDANDSSFVLFLFLGCLVVPLGVIAHCYGHILYSIRMLRCVEDL
                  190       200       210       220       230

                240       250       260       270       280       290
RHODOPSIN  QQQESATTQKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFA
           |  :         | ||:::::| :::|::::||:||:||  : | : : :|      | :  : :||
HG51       QTIQVIKILKYEKKLAKMCFLMIFTFLVCWMPYIVICFLVVNGHGHLVTPTISIVSYLFA
           240       250       260       270       280       290

                300       310       320       330       340
RHODOPSIN  KSAAIYNPVIYIMMNKQFRNCMLTTICCGKNPLGDDEASATVSKTETSQVAPA (SEQ ID NO:15)
           || ::|||||||::| ::||  :|  :|
HG51       KSNTVYNPVIYVFMIRKFRRSLLQLLCLRLLRCQRPAKDLPAAGSEMQIRPIVMSQKDGD
           300       310       320       330       340       350  (CONTAINED
                                                                 WITHIN SEQ.
                                                                  ID NO:2)
```

FIG. 5